## **WEST Search History**

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DATE: Thursday, September 27, 2007

Hide?	<u>Set</u> <u>Name</u>	Query	<u>Hit</u> Count
DB=PGPB, $USPT$ ; $PLUR=YES$ ; $OP=OR$			
	L11	19 and L10	. 13
	L10	long with sage	. 88
	L9	(organism or organism\$ or species or taxonom\$) same (complex\$ or divers\$)	61614
	L8	l6 and L7	. 8
	L7	(organism or organism\$ or species) same (complex\$ or divers\$)	61170
	L6	long with SAGE and genom\$ with (tag or tag\$)	14
	L5	(organism or organism\$) with (complex\$ or divers\$) and long with SAGE and genom\$ with (tag or tag\$)	8
	L4	(organism or organism\$) with (complex\$ or divers\$) and 13	2
	L3	long with SAGE same genom\$ with (tag or tag\$)	6
	L2	long with SAGE same signature with (tag or tag\$)	0
. 🗆	L1	long with SAGE same genom\$ with signature with (tag or tag\$)	0

END OF SEARCH HISTORY

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NEWS IPC8

TERMINAL (ENTER 1, 2, 3, OR ?):2

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         JUL 02 CHEMCATS accession numbers revised
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         JUL 02
                CA/CAplus enhanced with utility model patents from China
NEWS
         JUL 16 CAplus enhanced with French and German abstracts
NEWS
     7
NEWS
         JUL 18
                CA/CAplus patent coverage enhanced
         JUL 26
                USPATFULL/USPAT2 enhanced with IPC reclassification
NEWS
         JUL 30
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                USGENE now available on STN
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                 FSTA enhanced with new thesaurus edition
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                CA/CAplus enhanced with additional kind codes for granted
                 patents
NEWS 14
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                 patent family display formats from INPADOCDB
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                 USPATOLD now available on STN
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                 spectral property data
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                 STN AnaVist, Version 2.0, now available with Derwent
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                FORIS renamed to SOFIS
NEWS 20
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                 1967-1998
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                EMBASE, EMBAL, and LEMBASE reloaded with enhancements
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         SEP 24
NEWS EXPRESS
              19 SEPTEMBER 2007: CURRENT WINDOWS VERSION IS V8.2,
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FILE 'HOME' ENTERED AT 09:06:02 ON 27 SEP 2007

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0.21 0.21

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=> long (s) sage

L1354 LONG (S) SAGE

=> (organism or organism? or species or taxonom?) (s) (complex? or divers?) 2 FILES SEARCHED...

L2237306 (ORGANISM OR ORGANISM? OR SPECIES OR TAXONOM?) (S) (COMPLEX? OR DIVERS?)

=> 11 and 12

1 L1 AND L2

=> d ibib abs 13

ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2001:519183 BIOSIS DOCUMENT NUMBER: PREV200100519183

TITLE: High-throughput DNA sequencing and analysis of Micro-SAGE

libraries using MegaBACE 1000 to study hippocampal

transcriptome.

AUTHOR(S): Fan, Qing-Qing [Reprint author]; Jones, Gregg S.; Edwards,

John R.; Richlin-Zack, Kate; Kandel, Eric R. [Reprint

author]; Ju, Jinqyue

CORPORATE SOURCE: Center of Neurobiology, College of Physicians and Surgeons,

Howard Hughes Medical Institute, Columbia University, New

York, NY, USA

SOURCE: International Genome Sequencing and Analysis Conference,

(2000) Vol. 12, pp. 69. print.

Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September

12-15, 2000.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

Conference; (Meeting Poster)

LANGUAGE: English

Entered STN: 7 Nov 2001 ENTRY DATE:

## Last Updated on STN: 23 Feb 2002

AΒ Transcriptomes, the temporal and spatial expression patterns of genes in an organism, represent an important level of dynamic functional biological complexity. Studies of transcriptomes of different conditions will provide insight into the molecular basis of biological processes. High-throughput methods, such as Microarray and Serial Analysis of Gene Expression (SAGE) techniques, are highly effective in capturing snapshots of transcriptomes. In the study of genes related to long-term memory using Micro-SAGE, a modified SAGE method requiring much less starting materials, we have sequenced over 40,000 transcript tags from a mouse hippocampal SAGE library using MegaBACE 1000 capillary array DNA sequencers with DYEnamic ET Terminators. We incorporated a modified PCR protocol to amplify SAGE concatenants for high-throughput sequencing. We have also developed a post-sequencing data analysis protocol that includes Phred basecalling and Phrap assembly software to assign confidence scores and align sequences from both the 5' and 3' directions. We then used CONSED to perform the final manual editing of low quality regions in the electropherograms and thereby attained a high fidelity consensus sequence. The quality of our automated data analysis was evaluated against the manual analysis of more than 20,000 tags, and the results are comparable. Thus, we have developed a high-throughput DNA sequencing method for the analysis of SAGE libraries using MegaBACE 1000.

## => d his

(FILE 'HOME' ENTERED AT 09:06:02 ON 27 SEP 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT 09:06:41 ON 27 SEP 2007

L1 354 LONG (S) SAGE

L2 237306 (ORGANISM OR ORGANISM? OR SPECIES OR TAXONOM?) (S) (COMPLEX? OR L3 1 L1 AND L2

=> logoff hold
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SINCE FILE TOTAL ENTRY SESSION 33.26 33.47

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SESSION WILL BE HELD FOR 120 MINUTES
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